1

61

121

181

241

301

361

421

481

541

601

661

721

781

841

901

961

1021

1081

1141

1201

1261

1321

atgggtcacg gtgtcagctg cgcccgcacc ggcgacgagc acgacttctt ccgggcggcg cageteggeg acetegaege cetggeegee eteetegeeg eegaecette eetegetege egegecacce tetacgaceg ceteteegte etceacateg eegeegecaa tggeegeate gaggtgctct ccatgttctt ggatcgcggg gcgccgccgg acgcggtgaa tcggcacaag cagacgccgc tgatgctcgc ggccatgcac ggcaagatcg actgcgtgct caagctcctc caggccgacg caaatatett gatgttegae teggtgeaeg egaggaeetg eetecaceae geggegtaet aeggeeacgt egaetgeetg eaggeeatee tegeegeege geagaceaeg ccggtggccg actcatgggg tttcgcccgg ttcgtcaacg tcagggacga ccacggcgcc actecgetge atetegegge eaggeagggg eggeeggggt gegtgeaggt gttgetggag aacggcgcca ttgtgtcggc tttgacagga tcatatggct tccctggaag cacgtcgctt cattiggetg etegtagegg gaactiggat tgeateagga agetgettge etggggaget gatcggctcc aaagggattc ggctgggaga attccctatt ctgttgcgct gaaacggaac catggagcat gtgcagcttt gctgaaccct acatcagcag agcccatggt gtggccatcc ccacttaagt tcatcagtga gcttgaacca gaagctaagg ctctcctgga agcagctctg atggaagcca acagggagag ggagaagaaa atcctgaatg gcacaaagta ctccctgcca teccettege eeggtgatga eagtgeegat gaegatgeat geteagaggt gagegaeaeg gagetttget geatetgett egaceagget tgeaceattg aggtgeaaga etgtggaeat caaatgtgtg caccgtgcac gctggcactg tgctgtcaca acaaacccaa tccgacgacc etgacacege ecteacegge etgeceatte tgeeggggea geateteacg getggtggtg gcccaaacaa ggtctgcttg tgatcctgac aagccgtcat ccctgcagct cacccggaag cggtcgcgtc gatctcacaa cctcagtgag ggcagcagca gcttcaaagg gctaccttcg gccatgggct ccttctcaaa gcttggccgt ggctcgagcc gcatggcgga cagtgacagc agcaacctgg acaagcctga gcacgatcta tga

FIG. 1A

I	MGHGVSCART	10
II	GDEHD F FR AA HL G D LD A L AA LL AADPSLARRATLY	45
	DRLSV L HI AA AN G RIEV L SM FL DRGAPPDAVNR	78
	HKQTP L ML AA MH G K ID C V LK LL QADANILMFDSV	112
	HARTC L HH AA YY GHVD C L QA IL AAAQTTPVADSWGFARFVNVRDD	157
	HGATP L HL AA RQ G RPGC V QV LL ENGAIVSALTGSYGF	194
	PGSTS L HL AA RS GNLD CIRK LL AWGADRLQRDSAGRIPYSVA	236
	LKRNHGAC AA LLNPTSAEPM V WPSPLKFISELE	269
	PEAKA L LE AA LMEANREREKK I LNGTKYSLPSPSPG	305
III	DDSADDDACSEVS	318
IV	DTELCCICFDQACTIEVQDCGHQMCAPCTLALCCHNKPNPTTLTP	363
	PSPACPFCRGSISRLVVAQTRS	385
v	ACDPDKPSSLQLTRKRSRRSHNLSEGSSSFKGLPSAMGSFSKLGR	430
	GSSRMADSDSSNLDKPEHDL	450

XB3	CCICFDQACTIEVQDCGHQM-CAPCTLALCCHNKPNPTTLTPPSPACPFCR
c-Cbl	CKICAENDKDVKIEPCGHLM-CTSCLTSWQESEGQGCPFCR
IAP	CKICYVEECIVCFVPCGHVVACAKCALSVDKCPMCR

Andkyrdin ékorasin

XB3-N

ХВ3-С